

## SEQUENCE LISTING

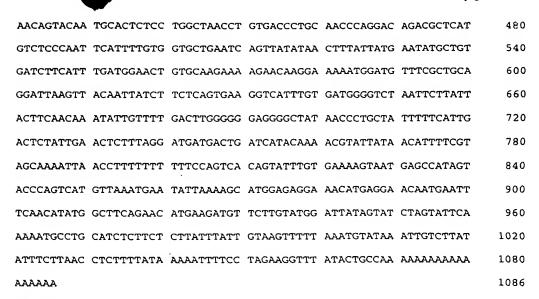
(1	)	GENERAL	INFORMATION
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- (i) APPLICANT: Bowman, Michael
- (ii) TITLE OF INVENTION: SECRETED PROTEIN BA3.1 AND POLYNUCLEOTIDES ENCODING SAME
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Genetics Institute, Inc.
  - (B) STREET: 87 CambridgePark Drive

  - (C) CITY: Cambridge
    (D) STATE: Massachusetts
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Sprunger, Suzanne A.(B) REGISTRATION NUMBER: 41,323

  - (C) REFERENCE/DOCKET NUMBER: GI5295A
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (617) 498-8284
    - (B) TELEFAX: (617) 876-5851
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1086 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGGCGGTAC	GATTTGTTAG	ACACAGGAGA	TGATCTTGAC	CCTGATATCA	TTAATATCCT	60
TCCTGCTTCT	CCAACTGGTT	CTCCTGTACA	TTCTCCAGGA	TCTCATTACC	CCCATGGAGG	120
TGATGCGGGC	AAGGGTCAGA	GTACTGATCG	GCTACTATCA	ACAGAACCTC	ATGAGGAAGT	180
ACCTAATATT	CTTCAGCAAC	CATTGGCCCT	TGGTTACTTT	GTATCAACTG	CCAAAGCAGG	240
TCCATTACCT	GACTGGTTCT	GGTCAGCATG	TCCTCAAGCA	CAATATCAGT	GTCCCCTTTT	300
TTCTTAAGGC	CTCTTTGCAC	CTCCACGTGC	CTTCAGTGCA	ATCTGACGAG	CTGCTTCACA	360
GTAAACACTC	CCACCCACTT	GACTCAAATC	AGACTTCAGA	TGTCCTCAGG	TTTGTTTTGG	420



## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 170 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Met Ile Leu Thr Leu Ile Ser Leu Ile Ser Phe Leu Leu Leu Gln Leu 1 5 10 15
- Val Leu Leu Tyr Ile Leu Gln Asp Leu Ile Thr Pro Met Glu Val Met 20 25 30
- Arg Ala Arg Val Arg Val Leu Ile Gly Tyr Tyr Gln Gln Asn Leu Met 35 40 45
- Arg Lys Tyr Leu Ile Phe Phe Ser Asn His Trp Pro Leu Val Thr Leu 50 55 60
- Tyr Gln Leu Pro Lys Gln Val His Tyr Leu Thr Gly Ser Gly Gln His 65 70 75 80
- Val Leu Lys His Asn Ile Ser Val Pro Phe Phe Leu Lys Ala Ser Leu 85 90 95
- His Leu His Val Pro Ser Val Gln Ser Asp Glu Leu Leu His Ser Lys 100 105 110
- His Ser His Pro Leu Asp Ser Asn Gln Thr Ser Asp Val Leu Arg Phe 115 120 125
- Val Leu Glu Gln Tyr Asn Ala Leu Ser Trp Leu Thr Cys Asp Pro Ala 130 135 140
- Thr Gln Asp Arg Arg Ser Cys Leu Pro Ile His Phe Val Val Leu Asn 145 150 155 160
- Gln Leu Tyr Asn Phe Ile Met Asn Met Leu 165